

=====

Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2009; month=11; day=25; hr=16; min=13; sec=19; ms=585;
]

=====

Application No: 10583415 Version No: 3.0

Input Set:**Output Set:**

Started: 2009-11-13 09:17:41.643
Finished: 2009-11-13 09:17:44.386
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 743 ms
Total Warnings: 15
Total Errors: 0
No. of SeqIDs Defined: 15
Actual SeqID Count: 15

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)

SEQUENCE LISTING

<110> MEYER, ROMAN
 SCHUTZ, MICHAEL
 GRALLERT, HOLGER
 GRASSL, RENATE
 MILLER, STEFAN

<120> ENDOTOXIN DETECTION METHOD

<130> DEBE:067US

<140> 10583415
 <141> 2009-11-13

<150> PCT/DE2004/002778
 <151> 2004-12-20

<150> DE 103 60 844.3
 <151> 2003-12-20

<160> 15

<170> PatentIn version 3.3

<210> 1
 <211> 78
 <212> DNA
 <213> artificial sequence

<220>
 <223> Synthetic primer

<400> 1
 gaaggaacta gtcatatggc tagctggagc caccgcagc tcgaaaaagg cgccagtaat 60
 aatacatatc aacacggtt 78

<210> 2
 <211> 54
 <212> DNA
 <213> artificial sequence

<220>
 <223> Synthetic primer

<400> 2
 acgcgcaaag cttgtcgacg gatcctatca ttcttttacc ttaattatgt agtt 54

<210> 3
 <211> 78
 <212> DNA
 <213> artificial sequence

<220>
<223> Synthetic primer

<400> 3
gaaggaacta gtcatatggc ttgttggagc caccgcagc tcgaaaaagg cgccagtaat 60

aatacatatc aacacggtt 78

<210> 4
<211> 78
<212> DNA
<213> artificial sequence

<220>
<223> Synthetic primer

<400> 4
gaaggaacta gtcatatggc tagctggagc caccgcagc tcgaaaaagg cgccagtaat 60

aatacatatc aacacggtt 78

<210> 5
<211> 19
<212> PRT
<213> artificial sequence

<220>
<223> Synthetic peptide

<400> 5

Met	Ala	Ser	Trp	Ser	His	Pro	Gln	Phe	Glu	Lys	Gly	Ala	Ser	Asn	Asn
1				5					10					15	

Thr Tyr Gln

<210> 6
<211> 19
<212> PRT
<213> artificial sequence

<220>
<223> Synthetic peptide

<400> 6

Met	Ala	Cys	Trp	Ser	His	Pro	Gln	Phe	Glu	Lys	Gly	Ala	Ser	Asn	Asn
1				5					10					15	

Thr Tyr Gln

<210> 7
<211> 19
<212> PRT
<213> artificial sequence

<220>
<223> Synthetic peptide

<400> 7

Met	Ala	Ser	Trp	Ser	His	Pro	Gln	Phe	Glu	Lys	Gly	Ala	Cys	Asn	Asn
1				5					10					15	

Thr Tyr Gln

<210> 8
<211> 539
<212> PRT
<213> artificial sequence

<220>
<223> Synthetic peptide

<400> 8

Met	Ala	Ser	Trp	Ser	His	Pro	Gln	Phe	Glu	Lys	Gly	Ala	Ser	Asn	Asn
1				5					10					15	

Thr	Tyr	Gln	His	Val	Ser	Asn	Glu	Ser	Arg	Tyr	Val	Lys	Phe	Asp	Pro
		20						25					30		

Thr	Asp	Thr	Asn	Phe	Pro	Pro	Glu	Ile	Thr	Asp	Val	Gln	Ala	Ala	Ile
	35						40					45			

Ala	Ala	Ile	Ser	Pro	Ala	Gly	Val	Asn	Gly	Val	Pro	Asp	Ala	Ser	Ser
50					55					60					

Thr	Thr	Lys	Gly	Ile	Leu	Phe	Leu	Ala	Thr	Glu	Gln	Glu	Val	Ile	Asp
65				70					75					80	

Gly	Thr	Asn	Asn	Thr	Lys	Ala	Val	Thr	Pro	Ala	Thr	Leu	Ala	Thr	Arg
		85						90					95		

Leu	Ser	Tyr	Pro	Asn	Ala	Thr	Glu	Ala	Val	Tyr	Gly	Leu	Thr	Arg	Tyr
		100						105					110		

Ser	Thr	Asp	Asp	Glu	Ala	Ile	Ala	Gly	Val	Asn	Asn	Glu	Ser	Ser	Ile	
		115					120					125				
Thr	Pro	Ala	Lys	Phe	Thr	Val	Ala	Leu	Asn	Asn	Val	Phe	Glu	Thr	Arg	
	130					135					140					
Val	Ser	Thr	Glu	Ser	Ser	Asn	Gly	Val	Ile	Lys	Ile	Ser	Ser	Leu	Pro	
145					150					155					160	
Gln	Ala	Leu	Ala	Gly	Ala	Asp	Asp	Thr	Thr	Ala	Met	Thr	Pro	Leu	Lys	
				165					170						175	
Thr	Gln	Gln	Leu	Ala	Val	Lys	Leu	Ile	Ala	Gln	Ile	Ala	Pro	Ser	Lys	
			180					185					190			
Asn	Ala	Ala	Thr	Glu	Ser	Glu	Gln	Gly	Val	Ile	Gln	Leu	Ala	Thr	Val	
		195					200					205				
Ala	Gln	Ala	Arg	Gln	Gly	Thr	Leu	Arg	Glu	Gly	Tyr	Ala	Ile	Ser	Pro	
	210					215					220					
Tyr	Thr	Phe	Met	Asn	Ser	Thr	Ala	Thr	Glu	Glu	Tyr	Lys	Gly	Val	Ile	
225					230					235					240	
Lys	Leu	Gly	Thr	Gln	Ser	Glu	Val	Asn	Ser	Asn	Asn	Ala	Ser	Val	Ala	
				245					250					255		
Val	Thr	Gly	Ala	Thr	Leu	Asn	Gly	Arg	Gly	Ser	Thr	Thr	Ser	Met	Arg	
			260					265						270		
Gly	Val	Val	Lys	Leu	Thr	Thr	Thr	Ala	Gly	Ser	Gln	Ser	Gly	Gly	Asp	
		275					280					285				
Ala	Ser	Ser	Ala	Leu	Ala	Trp	Asn	Ala	Asp	Val	Ile	His	Gln	Arg	Gly	
	290					295					300					
Gly	Gln	Thr	Ile	Asn	Gly	Thr	Leu	Arg	Ile	Asn	Asn	Thr	Leu	Thr	Ile	
305					310					315					320	
Ala	Ser	Gly	Gly	Ala	Asn	Ile	Thr	Gly	Thr	Val	Asn	Met	Thr	Gly	Gly	
				325					330						335	

Tyr	Ile	Gln	Gly	Lys	Arg	Val	Val	Thr	Gln	Asn	Glu	Ile	Asp	Arg	Thr	340	345	350
Ile	Pro	Val	Gly	Ala	Ile	Met	Met	Trp	Ala	Ala	Asp	Ser	Leu	Pro	Ser	355	360	365
Asp	Ala	Trp	Arg	Phe	Cys	His	Gly	Gly	Thr	Val	Ser	Ala	Ser	Asp	Cys	370	375	380
Pro	Leu	Tyr	Ala	Ser	Arg	Ile	Gly	Thr	Arg	Tyr	Gly	Gly	Ser	Ser	Ser	385	390	395
Asn	Pro	Gly	Leu	Pro	Asp	Met	Arg	Gly	Leu	Phe	Val	Arg	Gly	Ser	Gly	405	410	415
Arg	Gly	Ser	His	Leu	Thr	Asn	Pro	Asn	Val	Asn	Gly	Asn	Asp	Gln	Phe	420	425	430
Gly	Lys	Pro	Arg	Leu	Gly	Val	Gly	Cys	Thr	Gly	Gly	Tyr	Val	Gly	Glu	435	440	445
Val	Gln	Lys	Gln	Gln	Met	Ser	Tyr	His	Lys	His	Ala	Gly	Gly	Phe	Gly	450	455	460
Glu	Tyr	Asp	Asp	Ser	Gly	Ala	Phe	Gly	Asn	Thr	Arg	Arg	Ser	Asn	Phe	465	470	475
Val	Gly	Thr	Arg	Lys	Gly	Leu	Asp	Trp	Asp	Asn	Arg	Ser	Tyr	Phe	Thr	485	490	495
Asn	Asp	Gly	Tyr	Glu	Ile	Asp	Pro	Ala	Ser	Gln	Arg	Asn	Ser	Arg	Tyr	500	505	510
Thr	Leu	Asn	Arg	Pro	Glu	Leu	Ile	Gly	Asn	Glu	Thr	Arg	Pro	Trp	Asn	515	520	525
Ile	Ser	Leu	Asn	Tyr	Ile	Ile	Lys	Val	Lys	Glu						530	535	

<210> 9
 <211> 527
 <212> PRT
 <213> artificial sequence

<220>
<223> Synthetic peptide

<400> 9

Met	Ser	Asn	Asn	Thr	Tyr	Gln	His	Val	Ser	Asn	Glu	Ser	Arg	Tyr	Val
1				5					10					15	
Lys	Phe	Asp	Pro	Thr	Asp	Thr	Asn	Phe	Pro	Pro	Glu	Ile	Thr	Asp	Val
			20					25						30	
Gln	Ala	Ala	Ile	Ala	Ala	Ile	Ser	Pro	Ala	Gly	Val	Asn	Gly	Val	Pro
		35						40					45		
Asp	Ala	Ser	Ser	Thr	Thr	Lys	Gly	Ile	Leu	Phe	Leu	Ala	Thr	Glu	Gln
	50						55				60				
Glu	Val	Ile	Asp	Gly	Thr	Asn	Asn	Thr	Lys	Ala	Val	Thr	Pro	Ala	Thr
65					70					75					80
Leu	Ala	Thr	Arg	Leu	Ser	Tyr	Pro	Asn	Ala	Thr	Glu	Ala	Val	Tyr	Gly
				85					90						95
Leu	Thr	Arg	Tyr	Ser	Thr	Asp	Asp	Glu	Ala	Ile	Ala	Gly	Val	Asn	Asn
				100					105					110	
Glu	Ser	Ser	Ile	Thr	Pro	Ala	Lys	Phe	Thr	Val	Ala	Leu	Asn	Asn	Val
		115						120				125			
Phe	Glu	Thr	Arg	Val	Ser	Thr	Glu	Ser	Ser	Asn	Gly	Val	Ile	Lys	Ile
	130						135					140			
Ser	Ser	Leu	Pro	Gln	Ala	Leu	Ala	Gly	Ala	Asp	Asp	Thr	Thr	Ala	Met
145					150					155					160
Thr	Pro	Leu	Lys	Thr	Gln	Gln	Leu	Ala	Val	Lys	Leu	Ile	Ala	Gln	Ile
				165					170					175	
Ala	Pro	Ser	Lys	Asn	Ala	Ala	Thr	Glu	Ser	Glu	Gln	Gly	Val	Ile	Gln
			180						185					190	
Leu	Ala	Thr	Val	Ala	Gln	Ala	Arg	Gln	Gly	Thr	Leu	Arg	Glu	Gly	Tyr
			195				200						205		

Ala Ile Ser Pro Tyr Thr Phe Met Asn Ser Thr Ala Thr Glu Glu Tyr
210 215 220

Lys Gly Val Ile Lys Leu Gly Thr Gln Ser Glu Val Asn Ser Asn Asn
225 230 235 240

Ala Ser Val Ala Val Thr Gly Ala Thr Leu Asn Gly Arg Gly Ser Thr
245 250 255

Thr Ser Met Arg Gly Val Val Lys Leu Thr Thr Thr Ala Gly Ser Gln
260 265 270

Ser Gly Gly Asp Ala Ser Ser Ala Leu Ala Trp Asn Ala Asp Val Ile
275 280 285

His Gln Arg Gly Gly Gln Thr Ile Asn Gly Thr Leu Arg Ile Asn Asn
290 295 300

Thr Leu Thr Ile Ala Ser Gly Gly Ala Asn Ile Thr Gly Thr Val Asn
305 310 315 320

Met Thr Gly Gly Tyr Ile Gln Gly Lys Arg Val Val Thr Gln Asn Glu
325 330 335

Ile Asp Arg Thr Ile Pro Val Gly Ala Ile Met Met Trp Ala Ala Asp
340 345 350

Ser Leu Pro Ser Asp Ala Trp Arg Phe Cys His Gly Gly Thr Val Ser
355 360 365

Ala Ser Asp Cys Pro Leu Tyr Ala Ser Arg Ile Gly Thr Arg Tyr Gly
370 375 380

Gly Thr Ser Ser Asn Pro Gly Leu Pro Asp Met Arg Gly Leu Phe Val
385 390 395 400

Arg Gly Ser Gly Arg Gly Ser His Leu Thr Asn Pro Asn Val Asn Gly
405 410 415

Asn Asp Gln Phe Gly Lys Pro Arg Leu Gly Val Gly Cys Thr Gly Gly
420 425 430

Tyr Val Gly Glu Val Gln Lys Gln Gln Met Ser Tyr His Lys His Ala

435 440 445

Gly Gly Phe Gly Glu Tyr Asp Asp Ser Gly Ala Phe Gly Asn Thr Arg
450 455 460

Arg Ser Asn Phe Val Gly Thr Arg Lys Gly Leu Asp Trp Asp Asn Arg
465 470 475 480

Ser Tyr Phe Thr Asn Asp Gly Tyr Glu Ile Asp Pro Ala Ser Gln Arg
485 490 495

Asn Ser Arg Tyr Thr Leu Asn Arg Pro Glu Leu Ile Gly Asn Glu Thr
500 505 510

Arg Pro Trp Asn Ile Ser Leu Asn Tyr Ile Ile Lys Val Lys Glu
515 520 525

<210> 10
<211> 527
<212> PRT
<213> artificial sequence

<220>
<223> Synthetic peptide

<400> 10

Met Ser Asn Asn Thr Tyr Gln His Val Ser Asn Glu Ser Arg Tyr Val
1 5 10 15

Lys Phe Asp Pro Thr Asp Thr Asn Phe Pro Pro Glu Ile Thr Asp Val
20 25 30

His Ala Ala Ile Ala Ala Ile Ser Pro Ala Gly Val Asn Gly Val Pro
35 40 45

Asp Ala Ser Ser Thr Thr Lys Gly Ile Leu Phe Ile Pro Thr Glu Gln
50 55 60

Glu Val Ile Asp Gly Thr Asn Asn Thr Lys Ala Val Thr Pro Ala Thr
65 70 75 80

Leu Ala Thr Arg Leu Ser Tyr Pro Asn Ala Thr Glu Thr Val Tyr Gly
85 90 95

Leu Thr Arg Tyr Ser Thr Asn Asp Glu Ala Ile Ala Gly Val Asn Asn
100 105 110

Glu Ser Ser Ile Thr Pro Ala Lys Phe Thr Val Ala Leu Asn Asn Ala
115 120 125

Phe Glu Thr Arg Val Ser Thr Glu Ser Ser Asn Gly Val Ile Lys Ile
130 135 140

Ser Ser Leu Pro Gln Ala Leu Ala Gly Ala Asp Asp Thr Thr Ala Met
145 150 155 160

Thr Pro Leu Lys Thr Gln Gln Leu Ala Ile Lys Leu Ile Ala Gln Ile
165 170 175

Ala Pro Ser Glu Thr Thr Ala Thr Glu Ser Asp Gln Gly Val Val Gln
180 185 190

Leu Ala Thr Val Ala Gln Val Arg Gln Gly Thr Leu Arg Glu Gly Tyr
195 200 205

Ala Ile Ser Pro Tyr Thr Phe Met Asn Ser Ser Ser Thr Glu Glu Tyr
210 215 220

Lys Gly Val Ile Lys Leu Gly Thr Gln Ser Glu Val Asn Ser Asn Asn
225 230 235 240

Ala Ser Val Ala Val Thr Gly Ala Thr Leu Asn Gly Arg Gly Ser Thr
245 250 255

Thr Ser Met Arg Gly Val Val Lys Leu Thr Thr Thr Ala Gly Ser Gln
260 265 270

Ser Gly Gly Asp Ala Ser Ser Ala Leu Ala Trp Asn Ala Asp Val Ile
275 280 285

Gln Gln Arg Gly Gly Gln Ile Ile Tyr Gly Thr Leu Arg Ile Glu Asp
290 295 300

Thr Phe Thr Ile Ala Asn Gly Gly Ala Asn Ile Thr Gly Thr Val Arg
305 310 315 320

Met Thr Gly Gly Tyr Ile Gln Gly Asn Arg Ile Val Thr Gln Asn Glu

	325		330		335
Ile Asp Arg Thr Ile Pro Val Gly Ala Ile Met Met Trp Ala Ala Asp					
	340		345		350
Ser Leu Pro Ser Asp Ala Trp Arg Phe Cys His Gly Gly Thr Val Ser					
	355		360		365
Ala Ser Asp Cys Pro Leu Tyr Ala Ser Arg Ile Gly Thr Arg Tyr Gly					
	370		375		380
Gly Asn Pro Ser Asn Pro Gly Leu Pro Asp Met Arg Gly Leu Phe Val					
385		390		395	400
Arg Gly Ser Gly Arg Gly Ser His Leu Thr Asn Pro Asn Val Asn Gly					
	405		410		415
Asn Asp Gln Phe Gly Lys Pro Arg Leu Gly Val Gly Cys Thr Gly Gly					
	420		425		430
Tyr Val Gly Glu Val Gln Ile Gln Gln Met Ser Tyr His Lys His Ala					
	435		440		445
Gly Gly Phe Gly Glu His Asp Asp Leu Gly Ala Phe Gly Asn Thr Arg					
	450		455		460
Arg Ser Asn Phe Val Gly Thr Arg Lys Gly Leu Asp Trp Asp Asn Arg					
465		470		475	480
Ser Tyr Phe Thr Asn Asp Gly Tyr Glu Ile Asp Pro Glu Ser Gln Arg					
	485		490		495
Asn Ser Lys Tyr Thr Leu Asn Arg Pro Glu Leu Ile Gly Asn Glu Thr					
	500		505		510
Arg Pro Trp Asn Ile Ser Leu Asn Tyr Ile Ile Lys Val Lys Glu					
	515		520		525

<210> 11
 <211> 518
 <212> PRT
 <213> artificial sequence

<220>

<223> Synthetic peptide

<400> 11

Met	Ser	Asn	Asn	Thr	Tyr	Gln	His	Val	Ser	Asn	Glu	Ser	Lys	Tyr	Val
1				5					10					15	

Lys	Phe	Asp	Pro	Val	Gly	Ser	Asn	Phe	Pro	Asp	Thr	Val	Thr	Thr	Val
			20					25					30		

Gln	Ser	Ala	Leu	Ser	Lys	Ile	Ser	Asn	Ile	Gly	Val	Asn	Gly	Ile	Pro
		35						40					45		

Asp	Ala	Ser	Met	Glu	Val	Lys	Gly	Ile	Ala	Met	Ile	Ala	Ser	Glu	Gln
	50						55				60				

Glu	Val	Leu	Asp	Gly	Thr	Asn	Asn	Ser	Lys	Ile	Val	Thr	Pro	Ala	Thr
65					70					75					80

Leu	Ala	Thr	Arg	Leu	Leu	Tyr	Pro	Asn	Ala	Thr	Glu	Thr	Lys	Tyr	Gly
				85					90					95	

Leu	Thr	Arg	Tyr	Ser	Thr	Asn	Glu	Glu	Thr	Leu	Glu	Gly	Ser	Asp	Asn
				100				105						110	

Asn	Ser	Ser	Ile	Thr	Pro	Gln	Lys	Leu	Lys	Tyr	His	Thr	Asp	Asp	Val
		115						120					125		

Phe	Gln	Asn	Arg	Tyr	Ser	Ser	Glu	Ser	Ser	Asn	Gly	Val	Ile	Lys	Ile
	130						135				140				

Ser	Ser	Thr	Pro	Ala	Ala	Leu	Ala	Gly	Val	Asp	Asp	Thr	Thr	Ala	Met
145					150					155					160

Thr	Pro	Leu	Lys	Thr	Gln	Lys	Leu	Ala	Ile	Lys	Leu	Ile	Ser	Gln	Ile
				165					170					175	

Ala	Pro	Ser	Glu	Asp	Thr	Ala	Ser	Glu	Ser	Val	Arg	Gly	Val	Val	Gln
			180						185						